CASE NO.: 1798

Title: SOYBEAN VARIETY XB16Q04

Anticipated Class: 800

Subclass: 200

Art Unit: 1638

FIELD OF INVENTION

This invention is in the field of soybean breeding, specifically relating to a soybean variety designated XB16Q04.

BACKGROUND OF INVENTION

The present invention relates to a new and distinctive soybean variety, designated XB16Q04 which has been the result of years of careful breeding and selection as part of a soybean breeding program. There are numerous steps in the development of any novel, desirable plant germplasm. Plant breeding begins with the analysis and definition of problems and weaknesses of the current germplasm, the establishment of program goals, and the definition of specific breeding objectives. The next step is selection of germplasm that possess the traits to meet the program goals. The goal is to combine in a single variety an improved combination of desirable traits from the parental germplasm. These important traits may include higher seed yield, resistance to diseases and insects, tolerance to drought and heat, and better agronomic qualities.

These processes, which lead to the final step of marketing and distribution, can take from six to twelve years from the time the first cross is made. Therefore, development of new varieties is a time-consuming process that requires precise forward planning, efficient use of resources, and a minimum of changes in direction.

Soybean (*Glycine max)*, is an important and valuable field crop. Thus, a continuing goal of soybean breeders is to develop stable, high yielding soybean varieties that are agronomically sound. The reasons for this goal are to maximize the amount of grain produced on the land used and to supply food for both animals and humans. To accomplish this goal, the soybean breeder must select and develop soybean plants that have the traits that result in superior varieties.

Pioneer soybean research staff creates over 500,000 potential new varieties each year. Of those new varieties, less than 50 and more commonly less than 25 are actually selected for commercial use.

The soybean is the world's leading source of vegetable oil and protein meal. The oil extracted from soybeans is used for cooking oil, margarine, and salad dressings. Soybean oil is composed of saturated, monounsaturated and polyunsaturated fatty acids. It has a typical composition of 11% palmitic, 4% stearic, 25% oleic, 50% linoleic and 9% linolenic fatty acid content ("Economic Implications of Modified Soybean Traits Summary Report", Iowa Soybean Promotion Board & American Soybean Association Special Report 92S, May 1990). Changes in fatty acid composition for improved oxidative stability and nutrition are constantly sought after. Industrial uses of soybean oil which is subjected to further processing include ingredients for paints, plastics, fibers, detergents, cosmetics, and lubricants. Soybean oil may be split, inter-esterified, sulfurized, epoxidized, polymerized, ethoxylated, or cleaved. Designing and producing soybean oil derivatives with improved functionality, oliochemistry, is a rapidly growing field. The typical mixture of triglycerides is usually split and separated into pure fatty acids, which are then combined with petroleum-derived alcohols or acids, nitrogen, sulfonates, chlorine, or with fatty alcohols derived from fats and oils.

Soybean is also used as a food source for both animals and humans. Soybean is widely used as a source of protein for animal feeds for poultry, swine and cattle. During processing of whole soybeans, the fibrous hull is removed and the oil is extracted. The remaining soybean meal is a combination of carbohydrates and approximately 50% protein.

For human consumption soybean meal is made into soybean flour which is processed to protein concentrates used for meat extenders or specialty pet foods. Production of edible protein ingredients from soybean offers a healthy, less expensive replacement for animal protein in meats as well as dairy-type products.

SUMMARY OF INVENTION

According to the invention, there is provided a novel soybean variety, designated XB16Q04. This invention thus relates to the seeds of soybean variety XB16Q04, to the plants of soybean XB16Q04, to plant parts of soybean variety XB16Q04 and to methods for producing a soybean plant produced by crossing soybean variety XB16Q04 with another soybean plant, using XB16Q04 as either the male or the female parent. This invention also relates to methods for introgressing a transgenic or mutant trait into soybean variety XB16Q04 and to the soybean plants and plant parts produced by those methods. This invention also relates to soybean varieties or breeding varieties and plant parts derived from soybean variety XB16Q04, to methods for producing other soybean varieties or plant parts derived from soybean variety XB16Q04 and to the soybean plants, varieties, and their parts derived from use of those methods. This invention further relates to soybean seeds, plants, and plant parts produced by crossing the soybean variety XB16Q04 with another soybean variety.

Definitions

Certain definitions used in the specification are provided below. Also in the examples which follow, a number of terms are used. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided:

ALLELE = any of one or more alternative forms of a genetic sequence. In a diploid cell or organism, the two alleles of a given sequence typically occupy corresponding loci on a pair of homologous chromosomes.

BACKCROSSING = Process in which a breeder crosses a progeny variety back to one of the parental genotypes one or more times.

BREEDING = The genetic manipulation of living organisms.

BREEDING CROSS. A cross to introduce new genetic material into a plant for the development of a new variety. For example, one could cross plant A with plant B,

wherein plant B would be genetically different from plant A. After the breeding cross, the resulting F1 plants could then be selfed or sibbed for one, two, three or more times (F1, F2, F3, etc.) until a new variety is developed. For clarification, such new variety would be within a pedigree distance of one breeding cross of plants A and B. The process described above would be referred to as one breeding cycle.

BU/A = Bushels per Acre. The seed yield in bushels/acre is the actual yield of the grain at harvest.

BSR = Brown Stem Rot Tolerance. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based on leaf symptoms of yellowing and necrosis caused by brown stem rot. A score of 9 indicates no symptoms. Visual scores range down to a score of 1 which indicates severe symptoms of leaf yellowing and necrosis.

CW = Canopy Width. This is visual observation of the canopy width from 1 to 9 comparing all genotypes in a given test. The higher the score the better the canopy width observed.

CNKR = Stem Canker Tolerance. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based upon premature plant death. A score of 9 indicates no symptoms, whereas a score of 1 indicates the entire experimental unit died very early.

COTYLEDON = A cotyledon is a type of seed leaf. The cotyledon contains the food storage tissues of the seed.

ELITE VARIETY = A variety that is sufficiently homozygous and homogeneous to be used for commercial grain production. An elite variety may also be used in further breeding.

EMBRYO = The embryo is the small plant contained within a mature seed.

EMGSC = Emergence Score. The percentage of emerged plants in a plot respective to the number of seeds planted.

F3 = This symbol denotes a generation resulting from the selfing of the F2 generation along with selection for type and rogueing of off-types. The "F" number is a term commonly used in genetics, and designates the number of the filial

generation. The "F3" generation denotes the offspring resulting from the selfing or self mating of members of the generation having the next lower "F" number, viz. the F2 generation.

FEC = Iron-deficiency Chlorosis. Plants are scored 1 to 9 based on visual observations. A score of 1 indicates the plants are dead or dying from iron-deficiency chlorosis, a score of 5 means plants have intermediate health with some leaf yellowing and a score of 9 means no stunting of the plants or yellowing of the leaves. Plots are usually scored in mid July.

FECL = Iron-deficiency Chlorosis. Plants are scored 1 to 9 based on visual observations. A score of 1 indicates the plants are dead or dying from iron-deficiency chlorosis, a score of 5 means plants have intermediate health with some leaf yellowing and a score of 9 means no stunting of the plants or yellowing of the leaves. Plots are scored around mid August.

FEY = Frogeye Tolerance. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based upon leaf lesions. A score of 9 indicates no lesions, whereas a score of 1 indicates severe leaf necrosis.

GENOTYPE = Refers to the genetic constitution of a cell or organism.

HABIT = This refers to the physical appearance of a plant. It can be determinate, semi-determinate, intermediate, or indeterminate. In soybeans, indeterminate varieties are those in which stem growth is not limited by formation of a reproductive structure (i.e., flowers, pods and seeds) and hence growth continues throughout flowering and during part of pod filling. The main stem will develop and set pods over a prolonged period under favorable conditions. In soybeans, determinate varieties are those in which stem growth ceases at flowering time. Most flowers develop simultaneously, and most pods fill at approximately the same time. The terms semi-determinate and intermediate are also used to describe plant habit and are defined in Bernard, R.L. 1972. “Two genes affecting stem termination in soybeans.” Crop Science 12:235-239; Woodworth, C.M. 1932. “Genetics and breeding in the improvement of the soybean.” Bull. Agric. Exp. Stn. (Illinois) 384:297-

404; Woodworth, C.M. 1933. “Genetics of the soybean.” J. Am. Soc. Agron. 25:36-51.

HERBRES = Herbicide Resistance. This indicates that the plant is more tolerant to the herbicide shown than the level of herbicide tolerance exhibited by wild type plants. A designation of RR indicates tolerance to glyphosate and a designation of STS indicates tolerance to sulfonylurea herbicides.

HGT = Plant Height. Plant height is taken from the top of the soil to top pod of the plant and is measured in inches.

HILUM = This refers to the scar left on the seed which marks the place where the seed was attached to the pod prior to it (the seed) being harvested.

HYPL = Hypocotyl Elongation. This score indicates the ability of the seed to emerge when planted 3" deep in sand pots and with a controlled temperature of 25° C. The number of plants that emerge each day are counted. Based on this data, each genotype is given a 1 to 9 score based on its rate of emergence and percent of emergence. A score of 9 indicates an excellent rate and percent of emergence, an intermediate score of 5 indicates average ratings and a 1 score indicates a very poor rate and percent of emergence.

HYPOCOTYL = A hypocotyl is the portion of an embryo or seedling between the cotyledons and the root. Therefore, it can be considered a transition zone between shoot and root.

LDGSEV = Lodging Resistance. Lodging is rated on a scale of 1 to 9. A score of 9 indicates erect plants. A score of 5 indicates plants are leaning at a 45° angle in relation to the ground and a score of 1 indicates plants are laying on the ground.

LEAFLETS = These are part of the plant shoot, and they manufacture food for the plant by the process of photosynthesis.

LINKAGE = Refers to a phenomenon wherein alleles on the same chromosome tend to segregate together more often than expected by chance if their transmission was independent.

LINKAGE DISEQUILIBRIUM = Refers to a phenomenon wherein alleles tend to remain together in linkage groups when segregating from parents to offspring, with a greater frequency than expected from their individual frequencies.

LLE = Linoleic Acid Percent. Linoleic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

LLN = Linolenic Acid Percent. Linolenic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

MAT ABS = Absolute Maturity. This term is defined as the length of time from planting to complete physiological development (maturity). The period from planting until maturity is reached is measured in days, usually in comparison to one or more standard varieties. Plants are considered mature when 95% of the pods have reached their mature color.

MATURITY GROUP = This refers to an agreed-on industry division of groups of varieties, based on the zones in which they are adapted primarily according to day length or latitude. They consist of very long day length varieties (Groups 000, 00, 0), and extend to very short day length varieties (Groups VII, VIII, IX, X).

OIL = Oil Percent. Soybean seeds contain a considerable amount of oil. Oil is measured by NIR spectrophotometry, and is reported on an as is percentage basis.

OLC = Oleic Acid Percent. Oleic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

PEDIGREE DISTANCE = Relationship among generations based on their ancestral links as evidenced in pedigrees. May be measured by the distance of the pedigree from a given starting point in the ancestry.

PERCENT IDENTITY. Percent identity as used herein refers to the comparison of the homozygous alleles of two soybean varieties. Percent identity is determined by comparing a statistically significant number of the homozygous alleles of two developed varieties. For example, a percent identity of 90% between soybean

variety 1 and soybean variety 2 means that the two varieties have the same allele at 90% of their loci.

PERCENT SIMILARITY. Percent similarity as used herein refers to the comparison of the homozygous alleles of a soybean variety such as XB16Q04 with another plant, and if the homozygous allele of XB16Q04 matches at least one of the alleles from the other plant then they are scored as similar. Percent similarity is determined by comparing a statistically significant number of loci and recording the number of loci with similar alleles as a percentage. A percent similarity of 90% between XB16Q04 and another plant means that XB16Q04 matches at least one of the alleles of the other plant at 90% of the loci.

PLANT. As used herein, the term "plant" includes reference to an immature or mature whole plant, including a plant from which seed or grain or anthers have been removed. Seed or embryo that will produce the plant is also considered to be the plant.

PLANT PARTS. As used herein, the term "plant parts" includes leaves, stems, roots, root tips, anthers, seed, grain, embryo, pollen, ovules, flowers, cotyledon, hypocotyl, pod, flower, shoot and stalk, tissue, cells and the like.

PLM = Palmitic Acid Percent. Palmitic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

POD = This refers to the fruit of a soybean plant. It consists of the hull or shell (pericarp) and the soybean seeds.

PRT = Phytophthora Tolerance. Tolerance to Phytophthora root rot is rated on a scale of 1 to 9, with a score of 9 being the best or highest tolerance ranging down to a score of 1 which indicates the plants have no tolerance to Phytophthora.

PRMMAT = Predicted Relative Maturity. Soybean maturities are divided into relative maturity groups. In the United States the most common maturity groups are 00 through VIII. Within maturity groups 00 through V are sub-groups. A sub-group is a tenth of a relative maturity group. Within narrow comparisons, the difference of a

tenth of a relative maturity group equates very roughly to a day difference in maturity at harvest.

PRO = Protein Percent. Soybean seeds contain a considerable amount of protein. Protein is generally measured by NIR spectrophotometry, and is reported on a dry weight basis.

PUBESCENCE = This refers to a covering of very fine hairs closely arranged on the leaves, stems and pods of the soybean plant.

RKI = Root-knot Nematode, Southern. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based upon digging plants to visually score the roots for presence or absence of galling. A score of 9 indicates that there is no galling of the roots, a score of 1 indicates large severe galling cover most of the root system which results in pre-mature death from decomposing of the root system.

RKA = Root-knot Nematode, Peanut. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based upon digging plants to look at the roots for presence or absence of galling. A score of 9 indicates that there is no galling of the roots, a score of 1 indicates large severe galling cover most of the root system which results in pre-mature death from decomposing of the root system.

SCN = Soybean Cyst Nematode Resistance. The score is based on resistance to a particular race of soybean cyst nematode, such as race 1, 2, 3, 5 or 14. Scores are visual observations of resistance as versus other genotypes in the test, with a higher score indicating a higher level of resistance.

SD VIG = Seedling Vigor. The score is based on the speed of emergence of the plants within a plot relative to other plots within an experiment. A score of 9 indicates that 90% of plants growing have expanded first leaves. A score of 1 indicates no plants have expanded first leaves.

SDS = Sudden Death Syndrome. Tolerance to Sudden Death Syndrome is rated on a scale of 1 to 9, with a score of 1 being very susceptible ranging up to a score of 9 being tolerant.

S/LB = Seeds per Pound. Soybean seeds vary in seed size, therefore, the number of seeds required to make up one pound also varies. This affects the pounds of seed required to plant a given area, and can also impact end uses.

SHATTR = Shattering. This refers to the amount of pod dehiscence prior to harvest. Pod dehiscence involves seeds falling from the pods to the soil. This is a visual score from 1 to 9 comparing all genotypes within a given test. A score of 9 means pods have not opened and no seeds have fallen out. A score of 5 indicates approximately 50% of the pods have opened, with seeds falling to the ground and a score of 1 indicates 100% of the pods are opened.

SHOOTS = These are a portion of the body of the plant. They consist of stems, petioles and leaves.

STC = Stearic Acid Percent. Stearic acid is one of the five most abundant fatty acids in soybean seeds. It is measured by gas chromatography and is reported as a percent of the total oil content.

WH MD = White Mold Tolerance. This is a visual disease score from 1 to 9 comparing all genotypes in a given test. The score is based upon observations of mycelial growth and death of plants. A score of 9 indicates no symptoms. Visual scores of 1 indicate complete death of the experimental unit.

Definitions for Area of Adaptability

When referring to area of adaptability, such term is used to describe the location with the environmental conditions that would be well suited for this soybean variety. Area of adaptability is based on a number of factors, for example: days to maturity, insect resistance, disease resistance, and drought resistance. Area of adaptability does not indicate that the soybean variety will grow in every location within the area of adaptability or that it will not grow outside the area. Area of adaptability may also be used to refer to the soil or growing conditions.

Midwest: Iowa and Missouri

Heartland: Illinois and the western half of Indiana

Plains: 2/3 of the eastern parts of South Dakota and Nebraska
North Central: Minnesota, Wisconsin, the Upper Peninsula of Michigan, and the eastern half of North Dakota
Mideast: Michigan, Ohio, and the eastern half of Indiana
Eastern: Pennsylvania, Delaware, Maryland, Rhode Island, New Jersey, Connecticut, Massachusetts, New York, Vermont, and Maine
Southern: Virginia, West Virginia, Tennessee, Kentucky, Arkansas, North Carolina, South Carolina, Georgia, Florida, Alabama, Mississippi, and Louisiana
Western: Texas, Kansas, Colorado, Oklahoma, New Mexico, Arizona, Utah, Nevada, California, Washington, Oregon, Montana, Idaho, Wyoming, the western half of North Dakota, and the western 1/3 South Dakota and Nebraska
PMG infested soils: soils containing *Phytophthora sojae*
Narrow rows: 7" and 15" row spacing
High yield environments: areas which lack normal stress for example they have sufficient rainfall, water drainage, low disease pressure, and low weed pressure
Tough environments: areas which have stress challenges, opposite of a high yield environment
SCN infected soils: soils containing soybean cyst nematode
other areas of adaptation include the soybean growing regions of Canada, tight clay soils, light sandy soils and no-till locations.

DETAILED DESCRIPTION OF INVENTION

The variety of the invention has shown uniformity and stability for all traits, as described in the following variety description information. It has been self-pollinated a sufficient number of generations, with careful attention to uniformity of plant type to ensure a sufficient level of homozygosity and phenotypic stability. The variety has been increased with continued observation for uniformity. No variant traits have been observed or are expected.

Soybean variety XB16Q04 is particularly adapted to the Plains, North Central and Western United States and Canada, and for use in PMG infected soils.

Soybean variety XB16Q04 demonstrates a valuable combination of traits, including exceptional yield potential, phytophthora resistance provided by the Rps1c gene, good iron deficiency chlorosis, and resistance to glyphosate herbicides.

Soybean variety XB16Q04 exhibits a relative maturity of 1 and a subgroup of approximately 6. A variety description of Soybean variety XB16Q04 is provided in Table 1. Traits reported are average values for all locations and years or samples measured.

Soybean variety XB16Q04, being substantially homozygous, can be reproduced by planting seeds of the variety, growing the resulting soybean plants under self-pollinating or sib-pollinating conditions, and harvesting the resulting seed, using techniques familiar to the agricultural arts.

TABLE 1
Variety Description Information
XB16Q04

PERFORMANCE CHARACTERISTICS		
		XB16Q04
General Characteristics		
Herbicide Resistance	RR,STS	RR
Avg. Harvest Standability	LDGSEV	5
Avg. Field Emergence	EMGSC	8
Avg. Hypocotyl Length	HYPLSC	8
Hypocotyl Length		L
Avg. Canopy Width (9 = wide)	CW	5
Avg. Shattering	SHATTR	9
Disease/Insect/Fungal Resistance		
Phytophthora Race 4		Suscept
Phytophthora Race 7		Resistant
Phytophthora Race 25		Suscept
Avg. Phytophthora Tolerance	PRT	5
Avg. Brown Stem Rot	BSR	
Avg. Iron Chlorosis	FEC	6
Avg. White Mold	WHMD	6
Avg. Cyst Nematode Race 1	SCN1	
Avg. Cyst Nematode Race 3	SCN3	
Avg. Cyst Nematode Race 5	SCN5	
Avg. Cyst Nematode Race 14	SCN14	
Avg. Sudden Death Syndrome	SDS	6
Avg. Root-knot Nematode-Southern	RKI	
Avg. Root-knot Nematode - Peanut	RKA	
Avg. Stem Canker	CNKR	
Avg. Frogeye Leaf Spot	FEY	

TABLE 1 CONTINUED
Variety Description Information
XB16Q04

Oil/Meal Type		
Avg. Seed Protein (% @ Dry Wgt Basis)	PROT	38.8
Avg. Seed Oil (% @ Dry Wgt Basis)	OILT	21.6
Avg. Seed Size (avg seeds/lb)	S/LB	
Color Characteristics		
Flower Color	FL	Purple
Pubescence Color	PU	Tawny
Hila Color	HI	Black
Pod Color	PD	Brown
Seed Coat Luster	SCL	
Leaf Color	LC	

Performance Examples of XB16Q04

In the examples that follow in Table 2, the traits and characteristics of soybean variety XB16Q04 are given in paired comparisons with the Pioneer varieties shown in the following tables. Traits reported are mean values for all locations and years where paired comparison data was obtained.

TABLE 2A
VARIETY COMPARISON
DATA FOR XB16Q04 vs. 91B52

Statistic	YIELD bu/a 60# ABS	MATABS count ABS	LDGSEV score ABS	HGT in ABS	FEC score ABS	EMGSC score ABS	SDVIG score ABS
91B52	34.4	119.2	7.2	30.1	5.8	8.3	5.3
XB16Q04	36.2	120.3	5.7	32.6	6.4	8	5.3
#Locs	23	11	6	3	8	2	2
#Reps	23	11	6	3	8	2	2
#Years	2	2	2	2	2	1	1
Abs. Diff	1.8	1.2	1.4	2.4	0.6	0.3	0
Prob	0.003	0.048	0.013	0.048	0.144	0.500	1.000

Statistic	OILPCT pct ABS	PROTN pct ABS	G/C count ABS
91B52	19.67	34.52	15.7
XB16Q04	19.21	34.15	17.7
#Locs	4	4	2
#Reps	4	4	2
#Years	1	1	1
Abs. Diff	0.46	0.38	2
Prob	0.136	0.361	0.320

TABLE 2B
VARIETY COMPARISON
DATA FOR XB16Q04 vs. 91B64

Statistic	YIELD bu/a 60# ABS	MATABS count ABS	LDGSEV score ABS	HGT in ABS	FEC score ABS	EMGSC score ABS	SDVIG score ABS
91B64	37.4	122.5	7	37.1	4.5	6	4.5
XB16Q04	37.4	121.2	5.7	32.6	6.6	8	5.3
#Locs	29	13	6	3	10	2	2
#Reps	29	13	6	3	10	2	2
#Years	3	3	2	2	3	1	1
Abs. Diff	0	1.3	1.3	4.6	2.1	2	0.8
Prob	0.992	0.149	0.010	0.078	0.000	1.000	0.605

Statistic	OILPCT pct ABS	PROTN pct ABS	G/C count ABS
91B64	19.81	33.34	17.1
XB16Q04	19.21	34.15	17.7
#Locs	4	4	2
#Reps	4	4	2
#Years	1	1	1
Abs. Diff	0.6	0.81	0.6
Prob	0.030	0.020	0.333

TABLE 2C
VARIETY COMPARISON
DATA FOR XB16Q04 vs. 91M40

Statistic	YIELD bu/a 60# ABS	MATABS count ABS	LDGSEV score ABS	HGT in ABS	FEC score ABS	EMGSC score ABS	SDVIG score ABS
91M40	36.7	115.5	6.7	32	6.7	6.7	4.2
XB16Q04	35.6	118.2	5.7	34.3	6.8	8	5.3
#Locs	15	7	5	2	3	2	2
#Reps	15	7	5	2	3	2	2
#Years	1	1	1	1	1	1	1
Abs. Diff	1.1	2.7	1.1	2.3	0.1	1.3	1.2
Prob	0.284	0.005	0.140	0.177	0.893	0.295	0.579

Statistic	OILPCT pct ABS	PROTN pct ABS
91M40	19.12	35.13
XB16Q04	19.21	34.15
#Locs	4	4
#Reps	4	4
#Years	1	1
Abs. Diff	0.09	0.98
Prob	0.754	0.056

TABLE 2D
VARIETY COMPARISON
DATA FOR XB16Q04 vs. 91M50

Statistic	YIELD bu/a 60# ABS	MATABS count ABS	LDGSEV score ABS	HGT in ABS	FEC score ABS	EMGSC score ABS	SDVIG score ABS
91M50	34.4	118.2	8	36	6.3	7.3	7.5
XB16Q04	35.6	118.2	5.7	34.3	6.3	8	5.3
#Locs	15	7	5	2	4	2	2
#Reps	15	7	5	2	4	2	2
#Years	1	1	1	1	1	1	1
Abs. Diff	1.2	0	2.3	1.7	0.1	0.7	2.2
Prob	0.392	0.953	0.010	0.126	0.944	0.295	0.234

Statistic	OILPCT pct ABS	PROTN pct ABS
91M50	18.52	35.19
XB16Q04	19.21	34.15
#Locs	4	4
#Reps	4	4
#Years	1	1
Abs. Diff	0.69	1.04
Prob	0.011	0.014

TABLE 2E
VARIETY COMPARISON
DATA FOR XB16Q04 vs. 91M51

Statistic	YIELD bu/a 60# ABS	MATABS count ABS	LDGSEV score ABS	HGT in ABS	FEC score ABS	EMGSC score ABS	SDVIG score ABS
91M51	35.3	117.5	8.1	33	6	7.3	3.7
XB16Q04	35.6	118.2	5.7	34.3	6.3	8	5.3
#Locs	15	7	5	2	4	2	2
#Reps	15	7	5	2	4	2	2
#Years	1	1	1	1	1	1	1
Abs. Diff	0.2	0.8	2.5	1.3	0.3	0.7	1.7
Prob	0.891	0.205	0.003	0.410	0.531	1.000	0.605

Statistic	OILPCT pct ABS	PROTN pct ABS
91M51	20.08	33.96
XB16Q04	19.21	34.15
#Locs	4	4
#Reps	4	4
#Years	1	1
Abs. Diff	0.87	0.19
Prob	0.001	0.565

FURTHER EMBODIMENTS OF THE INVENTION

Genetic Marker Profile Through SSR and First Generation Progeny

In addition to phenotypic observations, a plant can also be identified by its genotype. The genotype of a plant can be characterized through a genetic marker profile which can identify plants of the same variety or a related variety or be used to determine or validate a pedigree. Genetic marker profiles can be obtained by techniques such as Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) which are also referred to as Microsatellites, and Single Nucleotide Polymorphisms (SNPs). For example, see Cregan et. al, "An Integrated Genetic Linkage Map of the Soybean Genome" Crop Science 39:1464-1490 (1999), and Berry et. al., Assessing Probability of Ancestry Using Simple Sequence Repeat Profiles: Applications to Maize Inbred Lines and Soybean Varieties" Genetics 165:331-342 (2003), each of which are incorporated by reference herein in their entirety.

Particular markers used for these purposes are not limited to any particular set of markers, but are envisioned to include any type of marker and marker profile which provides a means of distinguishing varieties. One method of comparison is where only the loci for which XB16Q04 is homozygous are used. For example, one set of publicly available markers which could be used to screen and identify variety XB16Q04 is disclosed in Table 3.

TABLE 3

Soybean SSR Marker Set

Markers		
Sctt008	Satt372	Satt495
Satt328	Satt582	Satt523
Satt572	Satt389	Satt284
Satt165	Satt543	Satt513
Satt042	Satt186	Satt590
Satt300	Sct137	Satt150
Satt050	Satt213	Satt567
Satt385	Satt384	Satt540
Satt545	Satt598	Satt175
Satt225	Satt204	Satt551
Satt133	Satt602	Satt250
Satt411	Satt452	Satt336
Satt233	Satt193	Satt255
Satt327	Satt348	Satt234
Satt421	Satt144	Satt257
Satt470	Sat090	Satt358
Satt455	Satt594	Satt259
Satt409	Satt517	Satt420
Satt228	Sat117	Satt262
Sct188	Sct187	Satt478
Satt426	Satt353	Satt592
Satt509	Satt568	Satt153
Satt251	Sctt009	Satt216
Satt197	Satt279	Satt266
Satt303	Satt367	Satt412
Satt577	Satt127	Satt546
Satt467	Sctt012	Satt172
Sct034	Satt270	Sat104
Satt304	Satt243	Satt440
Satt601	Satt243	Satt249
Satt556	Satt243	Sct046
Satt122	Sct028	Satt596
Satt534	Satt357	Satt380
Satt142	Satt532	Satt183
Satt565	Satt221	Satt431
Sct186	Satt383	Satt102
Satt451	Satt295	Satt555
Satt227	Satt507	Satt441
Satt432	Satt147	Satt557
Satt457	Satt196	Satt475

Primers and PCR protocols for assaying these and other markers are disclosed in the Soybase (sponsored by the USDA Agricultural Research Service and Iowa State University) located at the world wide web at 129.186.26.94/SSR.html. In addition to being used for identification of soybean variety XB16Q04 and plant parts and plant cells of variety XB16Q04, the genetic profile may be used to identify a soybean plant produced through the use of XB16Q04 or to verify a pedigree for progeny plants produced through the use of XB16Q04. The genetic marker profile is also useful in breeding and developing backcross conversions.

The present invention comprises a soybean plant characterized by molecular and physiological data obtained from the representative sample of said variety deposited with the ATCC. Further provided by the invention is a soybean plant formed by the combination of the disclosed soybean plant or plant cell with another soybean plant or cell and comprising the homozygous alleles of the variety.

Means of performing genetic marker profiles using SSR polymorphisms are well known in the art. SSRs are genetic markers based on polymorphisms in repeated nucleotide sequences, such as microsatellites. A marker system based on SSRs can be highly informative in linkage analysis relative to other marker systems in that multiple alleles may be present. Another advantage of this type of marker is that, through use of flanking primers, detection of SSRs can be achieved, for example, by the polymerase chain reaction (PCR), thereby eliminating the need for labor-intensive Southern hybridization. The PCR detection is done by use of two oligonucleotide primers flanking the polymorphic segment of repetitive DNA. Repeated cycles of heat denaturation of the DNA followed by annealing of the primers to their complementary sequences at low temperatures, and extension of the annealed primers with DNA polymerase, comprise the major part of the methodology.

Following amplification, markers can be scored by gel electrophoresis of the amplification products. Scoring of marker genotype is based on the size of the amplified fragment as measured by base pair weight or molecular weight of the fragment. While variation in the primer used or in laboratory procedures can affect

the reported weight, relative values should remain constant regardless of the specific primer or laboratory used. When comparing varieties it is preferable if all SSR profiles are performed in the same lab.

Primers used are publicly available and may be found in the Soybase or Cregan supra. See also, PCT Publication No. WO 99/31964 Nucleotide Polymorphisms in Soybean, US 6,162,967 Positional Cloning of Soybean Cyst Nematode Resistance Genes, and US 2002/0129402A1 Soybean Sudden Death Syndrome Resistant Soybeans and Methods of Breeding and Identifying Resistant Plants, the disclosure of which are incorporated herein by reference.

The SSR profile of soybean plant XB16Q04 can be used to identify plants comprising XB16Q04 as a parent, since such plants will comprise the same homozygous alleles as XB16Q04. Because the soybean variety is essentially homozygous at all relevant loci, most loci should have only one type of allele present. In contrast, a genetic marker profile of an F1 progeny should be the sum of those parents, e.g., if one parent was homozygous for allele x at a particular locus, and the other parent homozygous for allele y at that locus, then the F1 progeny will be xy (heterozygous) at that locus. Subsequent generations of progeny produced by selection and breeding are expected to be of genotype x (homozygous), y (homozygous), or xy (heterozygous) for that locus position. When the F1 plant is selfed or sibbed for successive filial generations, the locus should be either x or y for that position.

In addition, plants and plant parts substantially benefiting from the use of XB16Q04 in their development, such as XB16Q04 comprising a backcross conversion, transgene, or genetic sterility factor, may be identified by having a molecular marker profile with a high percent identity to XB16Q04. Such a percent identity might be 95%, 96%, 97%, 98%, 99%, 99.5% or 99.9% identical to XB16Q04.

The SSR profile of XB16Q04 also can be used to identify essentially derived varieties and other progeny varieties developed from the use of XB16Q04, as well as cells and other plant parts thereof. Such plants may be developed using the markers identified in WO 00/31964, US 6,162,967 and US2002/0129402A1. Progeny plants

and plant parts produced using XB16Q04 may be identified by having a molecular marker profile of at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5% genetic contribution from soybean variety, as measured by either percent identity or percent similarity. Such progeny may be further characterized as being within a pedigree distance of XB16Q04, such as within 1,2,3,4 or 5 or less cross-pollinations to a soybean plant other than XB16Q04 or a plant that has XB16Q04 as a progenitor. Unique molecular profiles may be identified with other molecular tools such as SNPs and RFLPs.

While determining the SSR genetic marker profile of the plants described *supra*, several unique SSR profiles may also be identified which did not appear in either parent of such plant. Such unique SSR profiles may arise during the breeding process from recombination or mutation. A combination of several unique alleles provides a means of identifying a plant variety, an F1 progeny produced from such variety, and progeny produced from such variety.

Introduction of a new trait or locus into XB16Q04

Variety XB16Q04 represents a new base genetic variety into which a new locus or trait may be introgressed. Direct transformation and backcrossing represent two important methods that can be used to accomplish such an introgression. The term backcross conversion and single locus conversion are used interchangeably to designate the product of a backcrossing program.

Backcross Conversions of XB16Q04

A backcross conversion of XB16Q04 occurs when DNA sequences are introduced through backcrossing (Hallauer *et al,* 1988), with XB16Q04 utilized as the recurrent parent. Both naturally occurring and transgenic DNA sequences may be introduced through backcrossing techniques. A backcross conversion may produce a plant with a trait or locus conversion in at least two or more backcrosses, including at least 2 crosses, at least 3 crosses, at least 4 crosses, at least 5 crosses and the

like. Molecular marker assisted breeding or selection may be utilized to reduce the number of backcrosses necessary to achieve the backcross conversion. For example, see Openshaw, S.J. et al., Marker-assisted Selection in Backcross Breeding. In: Proceedings Symposium of the Analysis of Molecular Data, August 1994, Crop Science Society of America, Corvallis, OR, where it is demonstrated that a backcross conversion can be made in as few as two backcrosses.

The complexity of the backcross conversion method depends on the type of trait being transferred (single genes or closely linked genes as vs. unlinked genes), the level of expression of the trait, the type of inheritance (cytoplasmic or nuclear) and the types of parents included in the cross. It is understood by those of ordinary skill in the art that for single gene traits that are relatively easy to classify, the backcross method is effective and relatively easy to manage. (See Hallauer et al. in Corn and Corn Improvement, Sprague and Dudley, Third Ed. 1998). Desired traits that may be transferred through backcross conversion include, but are not limited to, sterility (nuclear and cytoplasmic), fertility restoration, nutritional enhancements, drought tolerance, nitrogen utilization, altered fatty acid profile, low phytate, industrial enhancements, disease resistance (bacterial, fungal or viral), insect resistance and herbicide resistance. In addition, an introgression site itself, such as an FRT site, Lox site or other site specific integration site, may be inserted by backcrossing and utilized for direct insertion of one or more genes of interest into a specific plant variety. In some embodiments of the invention, the number of loci that may be backcrossed into XB16Q04 is at least 1, 2, 3, 4, or 5 and/or no more than 6, 5, 4, 3, or 2. A single locus may contain several transgenes, such as a transgene for disease resistance that, in the same expression vector, also contains a transgene for herbicide resistance. The gene for herbicide resistance may be used as a selectable marker and/or as a phenotypic trait. A single locus conversion of site specific integration system allows for the integration of multiple genes at the converted loci.

The backcross conversion may result from either the transfer of a dominant allele or a recessive allele. Selection of progeny containing the trait of interest is accomplished by direct selection for a trait associated with a dominant allele.

Transgenes transferred via backcrossing typically function as a dominant single gene trait and are relatively easy to classify. Selection of progeny for a trait that is transferred via a recessive allele requires growing and selfing the first backcross generation to determine which plants carry the recessive alleles. Recessive traits may require additional progeny testing in successive backcross generations to determine the presence of the locus of interest. The last backcross generation is usually selfed to give pure breeding progeny for the gene(s) being transferred, although a backcross conversion with a stably introgressed trait may also be maintained by further backcrossing to the recurrent parent with selection for the converted trait.

Along with selection for the trait of interest, progeny are selected for the phenotype of the recurrent parent. The backcross is a form of inbreeding, and the features of the recurrent parent are automatically recovered after successive backcrosses. Poehlman, Breeding Field Crops, P. 204 (1987). Poehlman suggests from one to four or more backcrosses, but as noted above, the number of backcrosses necessary can be reduced with the use of molecular markers. Other factors, such as a genetically similar donor parent, may also reduce the number of backcrosses necessary. As noted by Poehlman, backcrossing is easiest for simply inherited, dominant and easily recognized traits.

One process for adding or modifying a trait or locus in soybean variety XB16Q04 comprises crossing XB16Q04 plants grown from XB16Q04 seed with plants of another soybean variety that comprise the desired trait or locus, selecting F1 progeny plants that comprise the desired trait or locus to produce selected F1 progeny plants, crossing the selected progeny plants with the XB16Q04 plants to produce backcross progeny plants, selecting for backcross progeny plants that have the desired trait or locus and the morphological characteristics of soybean variety XB16Q04 to produce selected backcross progeny plants; and backcrossing to XB16Q04 three or more times in succession to produce selected fourth or higher backcross progeny plants that comprise said trait or locus. The modified XB16Q04 may be further characterized as having the physiological and morphological

characteristics of soybean variety XB16Q04 listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions and/or may be characterized by percent similarity or identity to XB16Q04 as determined by SSR markers. The above method may be utilized with fewer backcrosses in appropriate situations, such as when the donor parent is highly related or markers are used in the selection step. Desired traits that may be used include those nucleic acids known in the art, some of which are listed herein, that will affect traits through nucleic acid expression or inhibition. Desired loci include the introgression of FRT, Lox and other sites for site specific integration, which may also affect a desired trait if a functional nucleic acid is inserted at the integration site.

In addition, the above process and other similar processes described herein may be used to produce first generation progeny soybean seed by adding a step at the end of the process that comprises crossing XB16Q04 with the introgressed trait or locus with a different soybean plant and harvesting the resultant first generation progeny soybean seed.

Transformation

The advent of new molecular biological techniques has allowed the isolation and characterization of genetic elements with specific functions, such as encoding specific protein products. Scientists in the field of plant biology developed a strong interest in engineering the genome of plants to contain and express foreign genetic elements, or additional, or modified versions of native or endogenous genetic elements in order to alter the traits of a plant in a specific manner. Any DNA sequences, whether from a different species or from the same species, that are inserted into the genome using transformation are referred to herein collectively as "transgenes". In some embodiments of the invention, a transformed variant of XB16Q04 may contain at least one transgene but could contain at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 and/or no more than 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2. Over the last fifteen to twenty years several methods for producing transgenic plants have been developed, and the present invention also relates to transformed versions of

the claimed soybean variety XB16Q04.

One embodiment of the invention is a process for producing soybean variety XB16Q04 further comprising a desired trait, said process comprising transforming a soybean plant of variety XB16Q04 with a transgene that confers a desired trait. Another embodiment is the product produced by this process. In one embodiment the desired trait may be one or more of herbicide resistance, insect resistance, disease resistance, decreased phytate, or modified fatty acid or carbohydrate metabolism. The specific gene may be any known in the art or listed herein, including; a polynucleotide conferring resistance to imidazolinone, sulfonylurea, glyphosate, glufosinate, triazine and benzonitrile; a polynucleotide encoding a bacillus thuringiensis polypeptide, a polynucleotide encoding phytase, FAD-2, FAD-3, galactinol synthase or a raffinose synthetic enzyme; or a polynucleotide conferring resistance to soybean cyst nematode, brown stem rot, phytophthora root rot, soybean mosaic virus or sudden death syndrome.

Numerous methods for plant transformation have been developed, including biological and physical plant transformation protocols. See, for example, Miki *et al.,* "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology,* Glick, B.R. and Thompson, J.E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 67-88 and Armstrong, "The First Decade of Maize Transformation: A Review and Future Perspective" (Maydica 44:101-109, 1999). In addition, expression vectors and *in vitro* culture methods for plant cell or tissue transformation and regeneration of plants are available. See, for example, Gruber *et al.,* "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology,* Glick, B.R. and Thompson, J.E. Eds. (CRC Press, Inc., Boca Raton, 1993) pages 89-119.

The most prevalent types of plant transformation involve the construction of an expression vector. Such a vector comprises a DNA sequence that contains a gene under the control of or operatively linked to a regulatory element, for example a promoter. The vector may contain one or more genes and one or more regulatory elements.

A genetic trait which has been engineered into the genome of a particular soybean plant using transformation techniques, could be moved into the genome of another variety using traditional breeding techniques that are well known in the plant breeding arts. For example, a backcrossing approach may be used to move a transgene from a transformed soybean variety into an already developed soybean variety, and the resulting backcross conversion plant would then comprise the transgene(s).

Various genetic elements can be introduced into the plant genome using transformation. These elements include, but are not limited to genes; coding sequences; inducible, constitutive, and tissue specific promoters; enhancing sequences; and signal and targeting sequences. For example, see the traits, genes and transformation methods listed in U.S. Patent 6,118,055.

With transgenic plants according to the present invention, a foreign protein can be produced in commercial quantities. Thus, techniques for the selection and propagation of transformed plants, which are well understood in the art, yield a plurality of transgenic plants that are harvested in a conventional manner, and a foreign protein then can be extracted from a tissue of interest or from total biomass. Protein extraction from plant biomass can be accomplished by known methods which are discussed, for example, by Heney and Orr, *Anal. Biochem.* 114: 92-6 (1981).

A genetic map can be generated, primarily via conventional Restriction Fragment Length Polymorphisms (RFLP), Polymerase Chain Reaction (PCR) analysis, Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP) that identifies the approximate chromosomal location of the integrated DNA molecule. For exemplary methodologies in this regard, see Glick and Thompson, METHODS IN PLANT MOLECULAR BIOLOGY AND BIOTECHNOLOGY 269-284 (CRC Press, Boca Raton, 1993).

Wang et al. discuss "Large Scale Identification, Mapping and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome", Science, 280:1077-1082, 1998, and similar capabilities are becoming increasingly available for the soybean genome. Map information concerning chromosomal location is useful for proprietary

protection of a subject transgenic plant. If unauthorized propagation is undertaken and crosses made with other germplasm, the map of the integration region can be compared to similar maps for suspect plants to determine if the latter have a common parentage with the subject plant. Map comparisons would involve hybridizations, RFLP, PCR, SSR and sequencing, all of which are conventional techniques. SNPs may also be used alone or in combination with other techniques.

Likewise, by means of the present invention, plants can be genetically engineered to express various phenotypes of agronomic interest. Through the transformation of soybean the expression of genes can be modulated to enhance disease resistance, insect resistance, herbicide resistance, agronomic, grain quality and other traits. Transformation can also be used to insert DNA sequences which control or help control male-sterility. DNA sequences native to soybean as well as non-native DNA sequences can be transformed into soybean and used to modulate levels of native or non-native proteins. Various promoters, targeting sequences, enhancing sequences, and other DNA sequences can be inserted into the genome for the purpose of modulating the expression of proteins. Reduction of the activity of specific genes (also known as gene silencing, or gene suppression) is desirable for several aspects of genetic engineering in plants.

Many techniques for gene silencing are well known to one of skill in the art, including but not limited to antisense technology (see, *e.g.*, Sheehy *et al.* (1988) *PNAS* USA 85:8805-8809; and U.S. Patent Nos. 5,107,065; 5,453, 566; and 5,759,829); co-suppression (*e.g.*, Taylor (1997) *Plant Cell* 9:1245; Jorgensen (1990) *Trends Biotech.* 8(12): 340-344; Flavell (1994) *PNAS* USA 91:3490-3496; Finnegan *et al.* (1994) *Bio/Technology* 12: 883-888; and Neuhuber *et al.* (1994) *Mol. Gen. Genet.* 244:230-241); RNA interference (Napoli *et al.* (1990) *Plant Cell* 2:279-289; U.S. Patent No. 5,034,323; Sharp (1999) *Genes Dev.* 13:139-141; Zamore *et al.* (2000) *Cell* 101:25-33; and Montgomery *et al.* (1998) *PNAS* USA 95:15502-15507), virus-induced gene silencing (Burton, *et al.* (2000) *Plant Cell* 12:691-705; and Baulcombe (1999) *Curr. Op. Plant Bio.* 2:109-113); target-RNA-specific ribozymes (Haseloff *et al.* (1988) *Nature* 334: 585-591); hairpin structures (Smith *et al.* (2000)

Nature 407:319-320; WO 99/53050; and WO 98/53083); ribozymes (Steinecke *et al.* ((1992) *EMBO J.* 11:1525; and Perriman *et al.* ((1993) *Antisense Res. Dev.* 3:253); oligonucleotide mediated targeted modification (*e.g.*, WO 03/076574 and WO 99/25853); Zn-finger targeted molecules (*e.g.*, WO 01/52620; WO 03/048345; and WO 00/42219); and other methods or combinations of the above methods known to those of skill in the art.

Exemplary transgenes useful for genetic engineering include, but are not limited to, those categorized below.

1. Transgenes That Confer Resistance To Insects or Disease And That Encode:

(A) Plant disease resistance genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. See, for example Jones et al., Science 266: 789 (1994) (cloning of the tomato Cf-9 gene for resistance to *Cladosporium fulvum*); Martin et al., Science 262: 1432 (1993) (tomato *Pto* gene for resistance to *Pseudomonas syringae* pv. tomato encodes a protein kinase); Mindrinos *et al.*, Cell 78: 1089 (1994) (*Arabidopsis RSP2* gene for resistance to *Pseudomonas syringae*). A plant resistant to a disease is one that is more resistant to a pathogen as compared to the wild type plant.

(B) A *Bacillus thuringiensis* protein, a derivative thereof or a synthetic polypeptide modeled thereon. See, for example, Geiser *et al., Gene* 48: 109 (1986), who disclose the cloning and nucleotide sequence of a *Bt* delta-endotoxin gene. Moreover, DNA molecules encoding delta-endotoxin genes can be purchased from American Type Culture Collection (Rockville, MD), for example, under ATCC Accession Nos. 40098, 67136, 31995 and 31998. Other examples of *Bacillus thuringiensis* transgenes being genetically engineered are given in the following patents and patent applications and hereby are incorporated by reference for this purpose: 5,188,960; 5,689,052; 5,880,275; WO 91/114778; WO 99/31248; WO

01/12731; WO 99/24581; WO 97/40162 and US Application Serial Nos. 10/032,717; 10/414,637; and 10/606,320.

(C) An insect-specific hormone or pheromone such as an ecdysteroid and juvenile hormone, a variant thereof, a mimetic based thereon, or an antagonist or agonist thereof. See, for example, the disclosure by Hammock et al., Nature 344: 458 (1990), of baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone.

(D) An insect-specific peptide which, upon expression, disrupts the physiology of the affected pest. For example, see the disclosures of Regan, *J. Biol. Chem.* 269: 9 (1994) (expression cloning yields DNA coding for insect diuretic hormone receptor), and Pratt *et al., Biochem. Biophys. Res. Comm.*163: 1243 (1989) (an allostatin is identified in *Diploptera puntata).* See also U.S. Patent No.5,266,317 to Tomalski *et al.,* who disclose genes encoding insect-specific toxins.

(E) An enzyme responsible for an hyperaccumulation of a monterpene, a sesquiterpene, a steroid, hydroxamic acid, a phenylpropanoid derivative or another non-protein molecule with insecticidal activity.

(F) An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule; for example, a glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase and a glucanase, whether natural or synthetic. See PCT application WO 93/02197 in the name of Scott et *al.,* which discloses the nucleotide sequence of a callase gene. DNA molecules which contain chitinase-encoding sequences can be obtained, for example, from the ATCC under Accession Nos. 39637 and 67152. See also Kramer *et al., Insect Biochem. Molec. Biol.*23: 691 (1993), who teach the nucleotide sequence of a cDNA encoding tobacco hookworm chitinase, and Kawalleck *et al., Plant Molec. Biol.* 21: 673 (1993), who provide the nucleotide sequence of the parsley *ubi*4-2 polyubiquitin gene.

(G) A molecule that stimulates signal transduction. For example, see the disclosure by Botella *et al., Plant Molec. Biol.* 24: 757 (1994), of nucleotide

sequences for mung bean calmodulin cDNA clones, and Griess *et al., Plant Physiol.*104: 1467 (1994), who provide the nucleotide sequence of a maize calmodulin cDNA clone.

(H) A hydrophobic moment peptide. See PCT application WO 95/16776 (disclosure of peptide derivatives of Tachyplesin which inhibit fungal plant pathogens) and PCT application WO 95/18855 (teaches synthetic antimicrobial peptides that confer disease resistance), the respective contents of which are hereby incorporated by reference for this purpose.

(I) A membrane permease, a channel former or a channel blocker. For example, see the disclosure by Jaynes et *al., Plant Sci.* 89: 43 (1993), of heterologous expression of a cecropin-beta lytic peptide analog to render transgenic tobacco plants resistant to *Pseudomonas solanacearum.*

(J) A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells imparts resistance to viral infection and/or disease development effected by the virus from which the coat protein gene is derived, as well as by related viruses. See Beachy *et al., Ann. Rev. Phytopathol.*28: 451 (1990). Coat protein-mediated resistance has been conferred upon transformed plants against alfalfa mosaic virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y, tobacco etch virus, tobacco rattle virus and tobacco mosaic virus. *Id.*

(K) An insect-specific antibody or an immunotoxin derived therefrom. Thus, an antibody targeted to a critical metabolic function in the insect gut would inactivate an affected enzyme, killing the insect. *Cf.* Taylor *et al.,* Abstract #497, SEVENTH INT'L SYMPOSIUM ON MOLECULAR PLANT-MICROBE INTERACTIONS (Edinburgh, Scotland, 1994) (enzymatic inactivation in transgenic tobacco via production of single-chain antibody fragments).

(L) A virus-specific antibody. See, for example, Tavladoraki *et al., Nature* 366: 469 (1993), who show that transgenic plants expressing recombinant antibody genes are protected from virus attack.

(M) A developmental-arrestive protein produced in nature by a pathogen or

a parasite. Thus, fungal endo alpha-1,4-D-polygalacturonases facilitate fungal colonization and plant nutrient release by solubilizing plant cell wall homo-alpha-1,4-D-galacturonase. See Lamb *et al., Bio/Technology* 10: 1436 (1992). The cloning and characterization of a gene which encodes a bean endopolygalacturonase-inhibiting protein is described by Toubart *et al., Plant J.* 2: 367 (1992).

(N) A developmental-arrestive protein produced in nature by a plant. For example, Logemann *et al., Bio/Technology* 10: 305 (1992), have shown that transgenic plants expressing the barley ribosome-inactivating gene have an increased resistance to fungal disease.

(O) Genes involved in the Systemic Acquired Resistance (SAR) Response and/or the pathogenesis related genes. Briggs, S., Current Biology, 5(2) (1995).

(P) Antifungal genes (Cornelissen and Melchers, Pl. Physiol. 101:709-712, (1993) and Parijs et al., Planta 183:258-264, (1991) and Bushnell et al., Can. J. of Plant Path. 20(2):137-149 (1998).

(Q) Detoxification genes, such as for fumonisin, beauvericin, moniliformin and zearalenone and their structurally related derivatives. For example, see US Patent No. 5,792,931.

(R) Cystatin and cysteine proteinase inhibitors.

(S) Defensin genes. See WO03000863.

(T) Genes conferring resistance to nematodes, and in particular soybean cyst nematodes. See *e.g.* PCT Application WO96/30517; PCT Application WO93/19181, WO 03/033651 and Urwin et. al., Planta 204:472-479 (1998).

(U) Genes that confer resistance to Phytophthora Root Rot, such as the Rps 1, Rps 1-a, Rps 1-b, Rps 1-c, Rps 1-d, Rps 1-e, Rps 1-k, Rps 2, Rps 3-a, Rps 3-b, Rps 3-c, Rps 4, Rps 5, Rps 6, Rps 7 and other Rps genes. See, for example, Shoemaker et al, Phytophthora Root Rot Resistance Gene Mapping in Soybean, Plant Genome IV Conference, San Diego, CA (1995).

(V) Genes that confer resistance to Brown Stem Rot, such as described in US 5,689, 035 and incorporated by reference for this purpose.

2. Transgenes That Confer Resistance To A Herbicide, For Example:

(A) A herbicide that inhibits the growing point or meristem, such as an imidazolinone or a sulfonylurea. Exemplary genes in this category code for mutant ALS and AHAS enzyme as described, for example, by Lee *et al.,EMBO J.* 7: 1241 (1988), and Miki *et al., Theor. Appl.Genet.* 80: 449 (1990), respectively. See also, U.S. Patent Nos. 5,605,011; 5,013,659; 5,141,870; 5,767,361; 5,731,180; 5,304,732; 4,761,373; 5,331,107; 5,928,937; and 5,378,824; and international publication WO 96/33270, which are incorporated herein by reference for this purpose.

(B) Glyphosate (resistance imparted by mutant 5-enolpyruvl-3-phosphikimate synthase (EPSP) and *aroA* genes, respectively) and other phosphono compounds such as glufosinate (phosphinothricin acetyl transferase (PAT) and *Streptomyces hygroscopicus* phosphinothricin acetyl transferase (*bar)* genes), and pyridinoxy or phenoxy proprionic acids and cycloshexones (ACCase inhibitor-encoding genes). See, for example, U.S. Patent No. 4,940,835 to Shah et al., which discloses the nucleotide sequence of a form of EPSPS which can confer glyphosate resistance. U.S. Patent No. 5,627,061 to Barry et al. also describes genes encoding EPSPS enzymes. See also U.S. Patent Nos. 6,248,876 B1; 6,040,497; 5,804,425; 5,633,435; 5,145,783; 4,971,908; 5,312,910; 5,188,642; 4,940,835; 5,866,775; 6,225,114 B1; 6,130,366; 5,310,667; 4,535,060; 4,769,061; 5,633,448; 5,510,471; Re. 36,449; RE 37,287 E; and 5,491,288; and international publications WO 97/04103; WO 97/04114; WO 00/66746; WO 01/66704; WO 00/66747 and WO 00/66748, which are incorporated herein by reference for this purpose. Glyphosate resistance is also imparted to plants that express a gene that encodes a glyphosate oxido-reductase enzyme as described more fully in U.S. Patent Nos. 5,776,760 and 5,463,175, which are incorporated herein by reference for this purpose. In addition glyphosate resistance can be imparted to plants by the over expression of genes encoding glyphosate N-acetyltransferase. See, for example, U.S. Application Serial Nos. 60/244,385; 60/377,175 and 60/377,719. A DNA molecule encoding a mutant *aro*A gene can be obtained under ATCC accession No. 39256, and the nucleotide sequence of the mutant gene is disclosed in U.S. Patent No. 4,769,061 to Comai.

European patent application No. 0 333 033 to Kumada *et* al. and U.S. Patent No. 4,975,374 to Goodman *et al.* disclose nucleotide sequences of glutamine synthetase genes which confer resistance to herbicides such as L-phosphinothricin. The nucleotide sequence of a phosphinothricin-acetyl-transferase gene is provided in European Patent No. 0 242 246 and 0 242 236 to Leemans *et al.* De Greef *et al., Bio/Technology* 7: 61 (1989), describe the production of transgenic plants that express chimeric *bar* genes coding for phosphinothricin acetyl transferase activity. See also, U.S. Patent Nos. 5,969,213; 5,489,520; 5,550,318; 5,874,265; 5,919,675; 5,561,236; 5,648,477; 5,646,024; 6,177,616 B1; and 5,879,903, which are incorporated herein by reference for this purpose. Exemplary genes conferring resistance to phenoxy proprionic acids and cycloshexones, such as sethoxydim and haloxyfop, are the *Acc1-S1, Acc1-S2* and *Acc1-S3* genes described by Marshall *et al., Theor. Appl. Genet.* 83: 435 (1992).

(C) A herbicide that inhibits photosynthesis, such as a triazine *(psbA* and *gs+* genes) and a benzonitrile (nitrilase gene). Przibilla *et al., Plant Cell* 3: 169 (1991), describe the transformation of *Chlamydomonas* with plasmids encoding mutant *psbA* genes. Nucleotide sequences for nitrilase genes are disclosed in U.S. Patent No. 4,810,648 to Stalker, and DNA molecules containing these genes are available under ATCC Accession Nos. 53435, 67441 and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes *et al., Biochem. J.* 285: 173 (1992).

(D) Acetohydroxy acid synthase, which has been found to make plants that express this enzyme resistant to multiple types of herbicides, has been introduced into a variety of plants (see, e.g., Hattori et al. (1995) Mol Gen Genet 246:419). Other genes that confer tolerance to herbicides include: a gene encoding a chimeric protein of rat cytochrome P4507A1 and yeast NADPH-cytochrome P450 oxidoreductase (Shiota et al. (1994) Plant PhysiolPlant Physiol 106:17), genes for glutathione reductase and superoxide dismutase (Aono et al. (1995) Plant Cell Physiol 36:1687, and genes for various phosphotransferases (Datta et al. (1992) Plant Mol Biol 20:619).

(E) Protoporphyrinogen oxidase (protox) is necessary for the production of chlorophyll, which is necessary for all plant survival. The protox enzyme serves as the target for a variety of herbicidal compounds. These herbicides also inhibit growth of all the different species of plants present, causing their total destruction. The development of plants containing altered protox activity which are resistant to these herbicides are described in U.S. Patent Nos. 6,288,306 B1; 6,282,837 B1; and 5,767,373; and international publication WO 01/12825, which are incorporated herein by reference for this purpose.

3. Transgenes That Confer Or Contribute To A Grain Trait, Such As:

(A) Modified fatty acid metabolism, for example, by

(1) Transforming a plant with an antisense gene of stearoyl-ACP desaturase to increase stearic acid content of the plant. See Knultzon *et al., Proc. Natl. Acad. Sci. USA* 89: 2624 (1992),

(2) Elevating oleic acid via FAD-2 gene modification and/or decreasing linolenic acid via FAD-3 gene modification (see U.S. Patents 6,063,947; 6,323,392; and WO 93/11245),

(3) Altering conjugated linolenic or linoleic acid content, such as in WO 01/12800,

(4) Modifying LEC1, AGP, Dek1, Superal1, and/or thioredoxin. For example, see WO 02/42424, WO 98/22604, WO 03/011015, US 6,423,886 and Rivera-Madrid, R. et. al. Proc. Natl. Acad. Sci. 92:5620-5624 (1995).

(B) Decreased phytate content, for example, by the

(1) Introduction of a phytase-encoding gene would enhance breakdown of phytate, adding more free phosphate to the transformed plant. For example, see Van Hartingsveldt *et al., Gene* 127: 87 (1993), for a disclosure of the nucleotide sequence of an *Aspergillus niger* phytase gene.

(2) Introduction of a gene that reduces phytate content. In maize, this, for example, could be accomplished, by cloning and then re-introducing DNA associated with one or more of the alleles, such as the LPA alleles, identified in

maize mutants characterized by low levels of phytic acid, such as in Raboy *et al., Maydica* 35: 383 (1990) and/or by altering inositol kinase activity as in WO 02/059324, US2003/0009011, WO 03/027243, US2003/0079247 and WO 99/05298.

(C) Modified carbohydrate composition effected, for example, by transforming plants with a gene coding for an enzyme that alters the branching pattern of starch. See Shiroza *et al., J. Bacteriol.* 170: 810 (1988) (nucleotide sequence of *Streptococcus mutans* fructosyltransferase gene), Steinmetz *et al., Mol. Gen. Genet.* 200: 220 (1985) (nucleotide sequence of *Bacillus subtilis* levansucrase gene), Pen *et al., Bio/Technology* 10: 292 (1992) (production of transgenic plants that express *Bacillus licheniformis* alpha-amylase), Elliot *et al., Plant Molec. Biol.* 21: 515 (1993) (nucleotide sequences of tomato invertase genes), Søgaard *et al., J. Biol. Chem.* 268: 22480 (1993) (site-directed mutagenesis of barley alpha -amylase gene), and Fisher *et al., Plant Physiol.* 102: 1045 (1993) (maize endosperm starch branching enzyme II). The fatty acid modification genes mentioned above may also be used to effect starch content and/or composition through the interrelationship of the starch and oil pathways.

(D) Altered antioxidant content or composition, such as alteration of tocopherol or tocotrienols. For example, see WO 00/68393 involving the manipulation of antioxidant levels through alteration of a phytl prenyl transferase and WO 03/082899 through alteration of a homogentisate geranyl geranyl transferase.

(E) Improved digestibility and/or starch extraction through modification of UDP-D-xylose 4-epimerase, Fragile 1 and 2, Ref1, HCHL, C4H, such as in WO 99/10498.

4. Genes that Control Male-sterility

(A) Introduction of a deacetylase gene under the control of a tapetum-specific promoter and with the application of the chemical N-Ac-PPT (WO 01/29237).

(B) Introduction of various stamen-specific promoters (WO 92/13956, WO 92/13957).

(C) Introduction of the barnase and the barstar gene (Paul et al. Plant Mol.

Biol. 19:611-622, 1992).

5. Genes that create a site for site specific DNA integration. This includes the introduction of FRT sites that may be used in the FLP/FRT system and/or Lox sites that may be used in the Cre/Loxp system. For example, see Lyznik, et al., Site-Specific Recombination for Genetic Engineering in Plants, Plant Cell Rep (2003) 21:925-932 and WO 99/25821, which are hereby incorporated by reference. Other systems that may be used include the Gin recombinase of phage Mu (Maeser et al., 1991), the Pin recombinase of E. coli (Enomoto et al., 1983), and the R/RS system of the pSR1 plasmid (Araki et al., 1992).

6. Genes that affect growth characteristics, such as drought tolerance and nitrogen utilization. For example, see WO 00/73475 where water use efficiency is modulated through alteration of malate.

Using XB16Q04 to develop other soybean varieties

Soybean varieties such as XB16Q04 are typically developed for use in seed and grain production. However, soybean varieties such as XB16Q04 also provide a source of breeding material that may be used to develop new soybean varieties. Plant breeding techniques known in the art and used in a soybean plant breeding program include, but are not limited to, recurrent selection, mass selection, bulk selection, mass selection, backcrossing, pedigree breeding, open pollination breeding, restriction fragment length polymorphism enhanced selection, genetic marker enhanced selection, making double haploids, and transformation. Often combinations of these techniques are used. The development of soybean varieties in a plant breeding program requires, in general, the development and evaluation of homozygous varieties. There are many analytical methods available to evaluate a new variety. The oldest and most traditional method of analysis is the observation of phenotypic traits but genotypic analysis may also be used.

Using XB16Q04 In a Breeding Program

This invention is directed to methods for producing a soybean plant by crossing a first parent soybean plant with a second parent soybean plant wherein either the first or second parent soybean plant is variety XB16Q04. The other parent may be any other soybean plant, such as a soybean plant that is part of a synthetic or natural population. Any such methods using soybean variety XB16Q04 are part of this invention: selfing, sibbing, backcrosses, mass selection, pedigree breeding, bulk selection, hybrid production, crosses to populations, and the like. These methods are well known in the art and some of the more commonly used breeding methods are described below. Descriptions of breeding methods can be found in one of several reference books (e.g., Allard, *Principles of Plant Breeding*, 1960; Simmonds, *Principles of Crop Improvement*, 1979; Sneep et al., 1979; Fehr, "Breeding Methods for Cultivar Development", Chapter 7, *Soybean Improvement, Production and Uses*, 2nd ed., Wilcox editor, 1987).

Pedigree Breeding

Pedigree breeding starts with the crossing of two genotypes, such as XB16Q04 and another soybean variety having one or more desirable characteristics that is lacking or which complements XB16Q04. If the two original parents do not provide all the desired characteristics, other sources can be included in the breeding population. In the pedigree method, superior plants are selfed and selected in successive filial generations. In the succeeding filial generations the heterozygous condition gives way to homogeneous varieties as a result of self-pollination and selection. Typically in the pedigree method of breeding, five or more successive filial generations of selfing and selection is practiced: F1 $\rightarrow$ F2; F2$\rightarrow$ F3; F3 $\rightarrow$ F4; F4 $\rightarrow$ F_5, etc. After a sufficient amount of inbreeding, successive filial generations will serve to increase seed of the developed variety. Preferably, the developed variety comprises homozygous alleles at about 95% or more of its loci.

In addition to being used to create a backcross conversion, backcrossing can also be used in combination with pedigree breeding. As discussed previously,

backcrossing can be used to transfer one or more specifically desirable traits from one variety, the donor parent, to a developed variety called the recurrent parent, which has overall good agronomic characteristics yet lacks that desirable trait or traits. However, the same procedure can be used to move the progeny toward the genotype of the recurrent parent but at the same time retain many components of the non-recurrent parent by stopping the backcrossing at an early stage and proceeding with selfing and selection. For example, a soybean variety may be crossed with another variety to produce a first generation progeny plant. The first generation progeny plant may then be backcrossed to one of its parent varieties to create a BC1 or BC2. Progeny are selfed and selected so that the newly developed variety has many of the attributes of the recurrent parent and yet several of the desired attributes of the non-recurrent parent. This approach leverages the value and strengths of the recurrent parent for use in new soybean varieties.

Therefore, an embodiment of this invention is a method of making a backcross conversion of soybean variety XB16Q04, comprising the steps of crossing a plant of soybean variety XB16Q04 with a donor plant comprising a desired trait, selecting an F1 progeny plant comprising the desired trait, and backcrossing the selected F1 progeny plant to a plant of soybean variety XB16Q04. This method may further comprise the step of obtaining a molecular marker profile of soybean variety XB16Q04 and using the molecular marker profile to select for a progeny plant with the desired trait and the molecular marker profile of XB16Q04. In one embodiment the desired trait is a mutant gene or transgene present in the donor parent.

Recurrent Selection and Mass Selection

Recurrent selection is a method used in a plant breeding program to improve a population of plants. XB16Q04 is suitable for use in a recurrent selection program. The method entails individual plants cross pollinating with each other to form progeny. The progeny are grown and the superior progeny selected by any number of selection methods, which include individual plant, half-sib progeny, full-sib progeny and selfed progeny. The selected progeny are cross pollinated with each other to

form progeny for another population. This population is planted and again superior plants are selected to cross pollinate with each other. Recurrent selection is a cyclical process and therefore can be repeated as many times as desired. The objective of recurrent selection is to improve the traits of a population. The improved population can then be used as a source of breeding material to obtain new varieties for commercial or breeding use, including the production of a synthetic cultivar. A synthetic cultivar is the resultant progeny formed by the intercrossing of several selected varieties.

Mass selection is a useful technique when used in conjunction with molecular marker enhanced selection. In mass selection seeds from individuals are selected based on phenotype or genotype. These selected seeds are then bulked and used to grow the next generation. Bulk selection requires growing a population of plants in a bulk plot, allowing the plants to self-pollinate, harvesting the seed in bulk and then using a sample of the seed harvested in bulk to plant the next generation. Also, instead of self pollination, directed pollination could be used as part of the breeding program.

Mutation Breeding

Mutation breeding is another method of introducing new traits into soybean variety XB16Q04. Mutations that occur spontaneously or are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation; such as X-rays, Gamma rays (e.g. cobalt 60 or cesium 137), neutrons, (product of nuclear fission by uranium 235 in an atomic reactor), Beta radiation (emitted from radioisotopes such as phosphorus 32 or carbon 14), or ultraviolet radiation (preferably from 2500 to 2900nm), or chemical mutagens (such as base analogues (5-bromo-uracil), related compounds (8-ethoxy caffeine), antibiotics (streptonigrin), alkylating agents (sulfur mustards, nitrogen mustards, epoxides, ethylenamines, sulfates, sulfonates, sulfones, lactones), azide,

hydroxylamine, nitrous acid, or acridines. Once a desired trait is observed through mutagenesis the trait may then be incorporated into existing germplasm by traditional breeding techniques. Details of mutation breeding can be found in "Principals of Cultivar Development" Fehr, 1993 Macmillan Publishing Company the disclosure of which is incorporated herein by reference. In addition, mutations created in other soybean plants may be used to produce a backcross conversion of XB16Q04 that comprises such mutation.

Breeding with Molecular Markers

Molecular markers, which includes markers identified through the use of techniques such as Isozyme Electrophoresis, Restriction Fragment Length Polymorphisms (RFLPs), Randomly Amplified Polymorphic DNAs (RAPDs), Arbitrarily Primed Polymerase Chain Reaction (AP-PCR), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs), may be used in plant breeding methods utilizing XB16Q04.

Isozyme Electrophoresis and RFLPs have been widely used to determine genetic composition. Shoemaker and Olsen, ((1993) Molecular Linkage Map of Soybean (*Glycine max* L. Merr.). p. 6.131-6.138. *In* S.J. O'Brien (ed.) Genetic Maps: Locus Maps of Complex Genomes. Cold Spring Harbor Laboratory Press. Cold Spring Harbor, New York.), developed a molecular genetic linkage map that consisted of 25 linkage groups with about 365 RFLP, 11 RAPD (random amplified polymorphic DNA), three classical markers, and four isozyme loci. See also, Shoemaker R.C. 1994 RFLP Map of Soybean. P. 299-309 In R.L. Phillips and I.K. Vasil (ed.) DNA-based markers in plants. Kluwer Academic Press Dordrecht, the Netherlands.

SSR technology is currently the most efficient and practical marker technology; more marker loci can be routinely used and more alleles per marker locus can be found using SSRs in comparison to RFLPs. For example Diwan and

Cregan, described a highly polymorphic microsatellite loci in soybean with as many as 26 alleles. (Diwan, N., and P.B. Cregan 1997 Automated sizing of fluorescent-labeled simple sequence repeat (SSR) markers to assay genetic variation in Soybean Theor. Appl. Genet. 95:220-225.) Single Nucleotide Polymorphisms may also be used to identify the unique genetic composition of the invention and progeny varieties retaining that unique genetic composition. Various molecular marker techniques may be used in combination to enhance overall resolution.

Soybean DNA molecular marker linkage maps have been rapidly constructed and widely implemented in genetic studies. One such study is described in Cregan et. al, "An Integrated Genetic Linkage Map of the Soybean Genome" Crop Science 39:1464-1490 (1999). Sequences and PCR conditions of SSR Loci in Soybean as well as the most current genetic map may be found in Soybase on the world wide web.

One use of molecular markers is Quantitative Trait Loci (QTL) mapping. QTL mapping is the use of markers, which are known to be closely linked to alleles that have measurable effects on a quantitative trait. Selection in the breeding process is based upon the accumulation of markers linked to the positive effecting alleles and/or the elimination of the markers linked to the negative effecting alleles from the plant's genome.

Molecular markers can also be used during the breeding process for the selection of qualitative traits. For example, markers closely linked to alleles or markers containing sequences within the actual alleles of interest can be used to select plants that contain the alleles of interest during a backcrossing breeding program. The markers can also be used to select for the genome of the recurrent parent and against the genome of the donor parent. Using this procedure can minimize the amount of genome from the donor parent that remains in the selected plants. It can also be used to reduce the number of crosses back to the recurrent parent needed in a backcrossing program. The use of molecular markers in the selection process is often called genetic marker enhanced selection.

Production of Double Haploids

The production of double haploids can also be used for the development of plants with a homozygous phenotype in the breeding program. For example, a soybean plant for which XB16Q04 is a parent can be used to produce double haploid plants. Double haploids are produced by the doubling of a set of chromosomes (1N) from a heterozygous plant to produce a completely homozygous individual. For example, see Wan et al., "Efficient Production of Doubled Haploid Plants Through Colchicine Treatment of Anther-Derived Maize Callus", Theoretical and Applied Genetics, 77:889-892, 1989 and US2003/0005479. This can be advantageous because the process omits the generations of selfing needed to obtain a homozygous plant from a heterozygous source.

Thus, an embodiment of this invention is a process for making a substantially homozygous XB16Q04 progeny plant by producing or obtaining a seed from the cross of XB16Q04 and another soybean plant and applying double haploid methods to the F1 seed or F1 plant or to any successive filial generation. Based on studies in maize and currently being conducted in soybean, such methods would decrease the number of generations required to produce a variety with similar genetics or characteristics to XB16Q04. See Bernardo, R. and Kahler, A.L., Theor. Appl. Genet. 102:986-992, 2001.

In particular, a process of making seed retaining the molecular marker profile of soybean variety XB16Q04 is contemplated, such process comprising obtaining or producing F1 seed for which soybean variety XB16Q04 is a parent, inducing doubled haploids to create progeny without the occurrence of meiotic segregation, obtaining the molecular marker profile of soybean variety XB16Q04, and selecting progeny that retain the molecular marker profile of XB16Q04.

Use Of XB16Q04 In Tissue Culture

This invention is also directed to the use of variety XB16Q04 in tissue culture. Tissue culture of various tissues of soybeans and regeneration of plants therefrom is well known and widely published. For example, reference may be had to

Komatsuda, T. et al., "Genotype X Sucrose Interactions for Somatic Embryogenesis in Soybean," Crop Sci. 31:333-337 (1991); Stephens, P.A. et al., "Agronomic Evaluation of Tissue-Culture-Derived Soybean Plants," Theor. Appl. Genet. (1991) 82:633-635; Komatsuda, T. et al., "Maturation and Germination of Somatic Embryos as Affected by Sucrose and Plant Growth Regulators in Soybeans *Glycine gracilis* Skvortz and *Glycine max* (L.) Merr.," Plant Cell, Tissue and Organ Culture, 28:103-113 (1992); Dhir, S. et al., "Regeneration of Fertile Plants from Protoplasts of Soybean (*Glycine max* L. Merr.): Genotypic Differences in Culture Response," Plant Cell Reports (1992) 11:285-289; Pandey, P. et al., "Plant Regeneration from Leaf and Hypocotyl Explants of *Glycine wightii* (W. and A.) VERDC. *var. longicauda*," Japan J. Breed. 42:1-5 (1992); and Shetty, K., et al., "Stimulation of In Vitro Shoot Organogenesis in *Glycine max* (Merrill.) by Allantoin and Amides," Plant Science 81:(1992) 245-251; as well as U.S. Patent 5,024,944, issued June 18, 1991 to Collins et al. and U.S. Patent 5,008,200, issued April 16, 1991 to Ranch et al., the disclosures of which are hereby incorporated herein in their entirety by reference. Thus, another aspect of this invention is to provide cells which upon growth and differentiation produce soybean plants having the physiological and morphological characteristics of soybean variety XB16Q04.

Progeny plants

All plants produced by the use of the methods described herein and that retain the unique genetic or trait combinations of XB16Q04 are within the scope of the invention. Progeny of the breeding methods described herein may be characterized in any number of ways, such as by traits retained in the progeny, pedigree and/or molecular markers. Combinations of these methods of characterization may be used.

Breeders of ordinary skill in the art have developed the concept of an "essentially derived variety", which is defined in 7 U.S.C. § 2104(a)(3) of the Plant Variety Protection Act and is hereby incorporated by reference. Varieties and plants that are essentially derived from XB16Q04 are within the scope of the invention.

Pedigree is a method used by breeders of ordinary skill in the art to describe the varieties. Varieties that are more closely related by pedigree are likely to share common genotypes and combinations of phenotypic characteristics. All breeders of ordinary skill in the art maintain pedigree records of their breeding programs. These pedigree records contain a detailed description of the breeding process, including a listing of all parental varieties used in the breeding process and information on how such variety was used. One embodiment of this invention is progeny plants and parts thereof with at least one ancestor that is XB16Q04, and more specifically, where the pedigree of the progeny includes 1, 2, 3, 4, and/or 5 or less breeding crosses to a soybean plant other than XB16Q04 or a plant that has XB16Q04 as a parent or other progenitor. A breeder of ordinary skill in the art would know if XB16Q04 were used in the development of a progeny variety, and would also know how many crosses to a variety other than XB16Q04 or variety with XB16Q04 as a parent or other progenitor were made in the development of any progeny variety.

Molecular markers also provide a means by which those of ordinary skill in the art characterize the similarity or differences of two varieties. Using the breeding methods described herein, one can develop individual plants, plant cells, and populations of plants that retain at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.5% genetic contribution from soybean variety XB16Q04, as measured by either percent identity or percent similarity. In pedigree analysis the percentage genetic contribution may not be actually known, but on average 50% of the starting germplasm would be expected to be passed to the progeny variety after one cross to another variety, 25% after another cross to a different variety, and so on. With backcrossing, the expected contribution of XB16Q04 after 2, 3, 4 and 5 doses (or 1, 2, 3 and 4 backcrosses) would be 75%, 87.5%, 93.75% and 96.875% respectively. Actual genetic contribution may be much higher than the genetic contribution expected by pedigree,

especially if molecular markers are used in selection. Molecular markers could also be used to confirm and/or determine the pedigree of the progeny variety.

Traits are also used by those of ordinary skill in the art to characterize progeny. Traits are commonly evaluated at a significance level, such as a 1%, 5% or 10% significance level, when measured in plants grown in the same environmental conditions. For example, a backcross conversion of XB16Q04 may be characterized as having the same morphological and physiological traits as XB16Q04. The traits used for comparison may be any or all of the traits shown in Table 1 or Table 2. Environmental conditions should be appropriate for the traits or traits being evaluated. Sufficient selection pressure should be present for optimum measurement of traits of interest such as herbicide, insect or disease resistance. Similarly, an introgressed trait conversion of XB16Q04 for resistance, such as herbicide resistance, should not be compared to XB16Q04in the presence of the herbicide when comparing non-resistance related traits such as plant height and yield.

The population of plants produced at each and any cycle of breeding is also an embodiment of the invention, and on average each such population would predictably consist of plants containing approximately 50% of its genes from variety XB16Q04 in the first breeding cycle, 25% of its genes from variety XB16Q04 in the second breeding cycle, 12.5% of its genes from variety XB16Q04 in the third breeding cycle, 6.25% in the fourth breeding cycle, and so on. However, in each case the use of variety XB16Q04 provides a benefit, because linkage groups of XB16Q04 are retained in the progeny varieties. Specifically, an embodiment of the invention is a process for making a population of XB16Q04 progeny plants comprising obtaining or producing a first generation progeny seed comprising the plant of XB16Q04 as a parent, growing said first generation progeny seed to produce first generation plants, obtaining self or sib pollinated seed from said first generation plants, and growing the self or sib pollinated seed to obtain a population of XB16Q04 progeny plants.

The population of XB16Q04 progeny soybean plants produced by this method will retain the expected genetic contribution of XB16Q04 described above. A variety selected from the population of XB16Q04 progeny plants produced by this method is an embodiment, and such variety may be further characterized by its molecular marker identity or similarity to XB16Q04.

In this manner, the invention encompasses a process for making a substantially homozygous XB16Q04 progeny plant comprising the steps of obtaining or producing a first generation progeny seed wherein a parent of said first generation progeny seed is a plant of variety XB16Q04, growing said first generation progeny seed to produce a first generation plant and obtaining self or sib pollinated seed from said first generation soybean plant, and producing successive filial generations to obtain a substantially homozygous XB16Q04 progeny plant. Also an embodiment of this invention is the substantially homozygous XB16Q04 progeny plant produced by this method.

DEPOSITS

Applicant(s) will make a deposit of at least 2500 seeds of Soybean Variety XB16Q04 with the American Type Culture Collection (ATCC), Manassas, VA 20110 USA, ATCC Deposit No. _________. The seeds deposited with the ATCC on ____________ will be taken from the deposit maintained by Pioneer Hi-Bred International, Inc., 800 Capital Square, 400 Locust Street, Des Moines, Iowa 50309-2340 since prior to the filing date of this application. Access to this deposit will be available during the pendency of the application to the Commissioner of Patents and Trademarks and persons determined by the Commissioner to be entitled thereto upon request. Upon allowance of any claims in the application, the Applicant(s) will make the deposit available to the public pursuant to 37 CFR 1.808. This deposit of Soybean Variety XB16Q04 will be maintained in the ATCC depository, which is a public depository, for a period of 30 years, or 5 years after the most recent request, or for the enforceable life of the patent, whichever is longer, and will be replaced if it becomes nonviable during that period. Additionally, Applicant(s) have or will satisfy all the requirements of 37 C.F.R. §§1.801 - 1.809, including providing an indication of the viability of the sample upon deposit. Applicant(s) have no authority to waive any restrictions imposed by law on the transfer of biological material or its transportation in commerce. Applicant(s) do not waive any infringement of their rights granted under this patent or under the Plant Variety Protection Act (7 USC 2321 et seq.).

All publications, patents and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All such publications, patents and patent applications are incorporated by reference herein for the purpose cited to the same extent as if each was specifically and individually indicated to be incorporated by reference herein.

The foregoing invention has been described in detail by way of illustration and example for purposes of clarity and understanding. As is readily apparent to one skilled in the art, the foregoing are only some of the methods and compositions that

illustrate the embodiments of the foregoing invention. It will be apparent to those of ordinary skill in the art that variations, changes, modifications and alterations may be applied to the compositions and/or methods described herein without departing from the true spirit, concept and scope of the invention.